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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU, HIROYUKI; MIKI, HIDEO; KAWAI, SHINJI; KIMURA, MICHIO; MATSUMOTO, TOMOAKI; KATSUURA, MIEKO; ENOMOTO, KOICHI; SATOH, YUSUKE
- (ii) TITLE OF INVENTION: A NOVEL PROTEIN AND PROCESS FOR PREPARING THE SAME
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS LLP
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/945,459
(B) FILING DATE: 09-DEC-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP96/01062
(B) FILING DATE: 19-APR-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/322403
(B) FILING DATE: 17-NOV-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/93664
(B) FILING DATE: 19-APR-1995
- (vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CHARLES A. MUSERLIAN
(B) REGISTRATION NUMBER: 19,683
(C) REFERENCE/DOCKET NUMBER: 146.1275

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 661-8000
(B) TELEFAX: (212) 661-8002
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMOSAPIENS
(F) TISSUE TYPE: FETUS

(ix) FEATURE:
(A) NAME/KEY: MP52
(B) LOCATION: 383 TO 501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys
1 5 10

Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His
15 20

Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile
25 30 35

Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
40 45

Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu
50 55 60

Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn
65 70

Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys
 75 80

Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
 85 90 95

Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr
 100 105

Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
 110 115

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATAATGCCAC TAGCAACTCG TCAGGGC
 GC(A/U/GC) outward
 Pro Leu Ala

27

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTCGACTAC CTGCAGCCAC ACGACT

26

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCA	CTG	GCC	ACT	CGC	CAG	GGC	AAG	CGA	CCC	AGC	AAG	36
Pro	Leu	Ala	Thr	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	
1				5					10			
AAC	CTT	AAG	GCT	CGC	TGC	AGT	CGG	AAG	GCA	CTG	CAT	72
Asn	Leu	Lys	Ala	Arg	Cys	Ser	Arg	Lys	Ala	Leu	His	
		15					20					
GTC	AAC	TTC	AAG	GAC	ATG	GGC	TGG	GAC	GAC	TGG	ATC	108
Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp	Asp	Trp	Ile	
25					30					35		
ATC	GCA	CCC	CTT	GAG	TAC	GAG	GCT	TTC	CAC	TGC	GAG	144
Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	
			40					45				
GGG	CTG	TGC	GAG	TTC	CCA	TTG	CGC	TCC	CAC	CTG	GAG	180
Gly	Leu	Cys	Glu	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	
	50					55					60	
CCC	ACG	AAT	CAT	GCA	GTC	ATC	CAG	ACC	CTG	ATG	AAC	216
Pro	Thr	Asn	His	Ala	Val	Ile	Gln	Thr	Leu	Met	Asn	
				65					70			
TCC	ATG	GAC	CCC	GAG	TCC	ACA	CCA	CCC	ACC	TGC	TGT	252
Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro	Thr	Cys	Cys	
		75					80					
GTG	CCC	ACG	CGA	CTG	AGT	CCC	ATC	AGC	ATC	CTC	TTC	288
Val	Pro	Thr	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	
85					90					95		
ATT	GAC	TCT	GCC	AAC	AAC	GTG	GTG	TAT	AAG	CAG	TAT	324
Ile	Asp	Ser	Ala	Asn	Asn	Val	Val	Tyr	Lys	Gln	Tyr	
			100					105				
GAG	GAC	ATG	GTC	GTG	GAG	TCG	TGT	GGC	TGC	AGG		357
Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg		
	110					115						